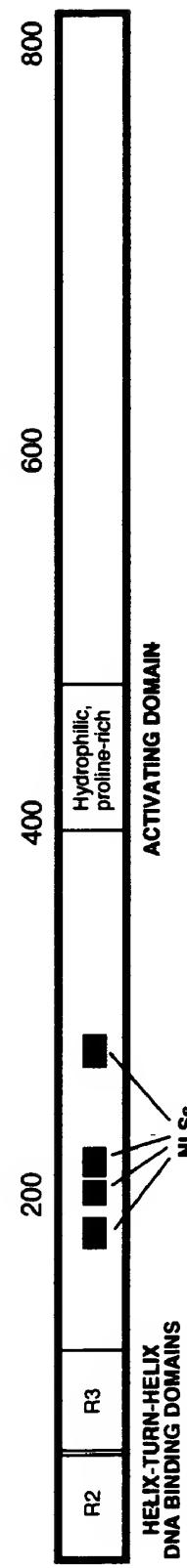


MPRIMIKGGVWRNTEDEILKAAVMKYGKNQWSRIASLLHRKSAKQCKARW 50
 YEWLDPISKTEWSREEEKLLHLAKLMPQTQWRTIAPIIGRTAAQCLEHY 100
 EFLLDKAAQRDNEEETTDDPRKLKPGEIDPNPETKPARPDPIDMDEDELE 150
 MLSEARARLANTQGKKAKRKAREKQLEEARRLAALQKRRELRAAGIEIQK 200
 KRKRKRGVDYNAEIPFEKKPALGFYDTSEENYQALDADFRKLQQQLDGE 250
 LRSEKEGRDRKKDKQHLKRKKESDLPSAILQTSGVSEFTKKRSKLVLPAP 300
 QISDAELQEVVKGQASEIARQTAEESGITNSASSTLLSEYNVTNNVAL 350
 RTPRTPASQDRILQEAQNLMALTNVDTPLKGGLNTPLHESDFSGVTPORO 400
 VVQTPNTVLSTPFRTPSNGAEGLTPRSQTTPKPVINSTPGRTPLRDKLNI 450
 NPEDGMADYSDPSYVKOMERESREHLRLGLLGLPAPKNDFEIVLPENAEK 500
 ELEEREIDDTYIEDAADVDARKQAIRDAERVKEMKRMHKAVQKDLPRPSE 550
 VNETILRPLNVEPPLTDLQKSEELIKKEMITMLHYDLLHHPYEPGNKKG 600
 KTVGFGTNNSEHITLEHNPYEKFSKEELKKAQDVLVQEMEVVKQGMSHG 650
 ELSSEAYNQVWEECYSQVLYLPGQSRYTRANLASKKDRIESLEKRLEINR 700
 GHMTTEAKRAAKMEKKMKILLGGYQSRAMGLMKQLNDLWDQIEQAHLELR 750
 TFEELKKHEDSAIPRRLECLKEDVQRQQEREKELQHRYADLLLEKETLKS 800
 KF*

Fig. 1A



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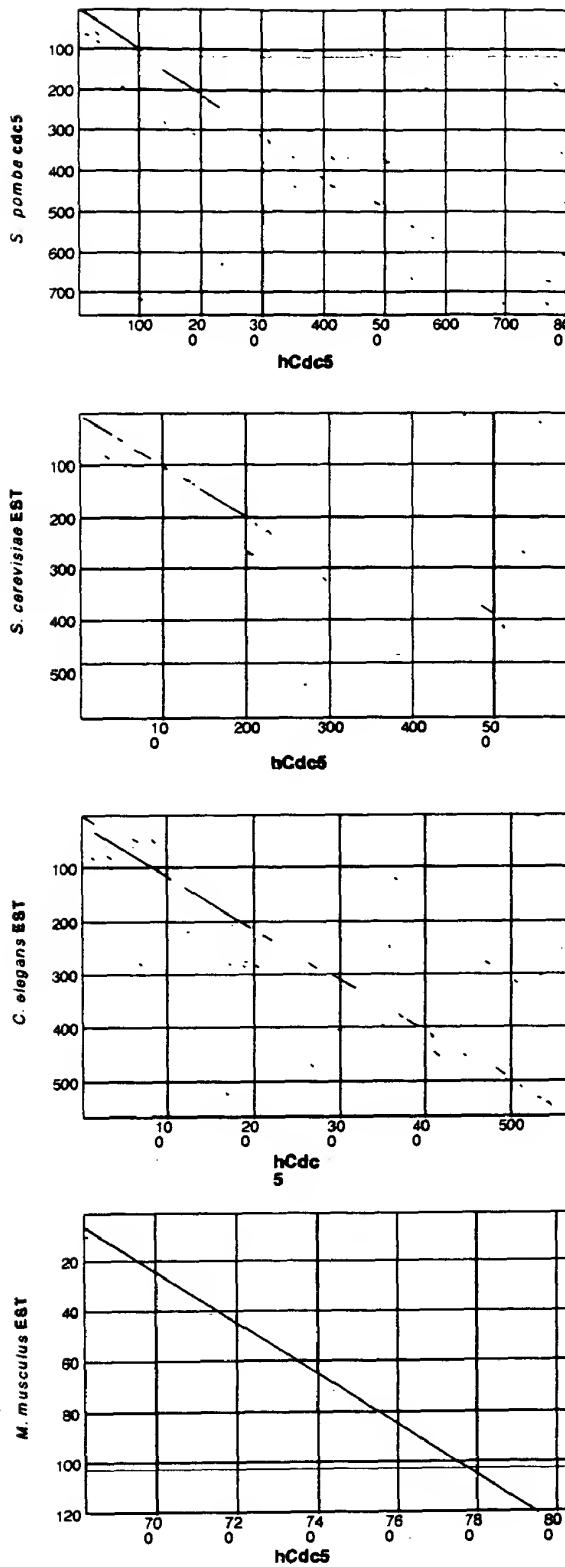


Fig. 2A

ICdc5	IKGGWWRNTEDEILKAAVMKYGKQWSRIASLLHRKSAKQCKARWYEWLDP	(6-56)
Spontaneous	IKGGAWKNTEDEILKAAVSKYGKQWARISSLLVWRKTPKQCKARWYEWLDP	(5-55)
bMyo	YIK-GPWTKEEDQKVIELVKKYGTQWTLIAKHLKGRQCRERWHNHLP	(88-137)
aMyo	IK-GPWTKEEDQRVIELVQKYGPKRWSLIAKHLKGRIGKQCRERWHNHLP	(87-136)
cMyo	IK-GPWTKEEDQRVIELVQKYGPKRWSVIAKHLKGRIGKQCRERWHNHLP	(92-141)

hCdc5
S.pombe cdc5
b-Myb
a-Myb
c-Myb

Fig. 2B

Fig. 2C

hCdc5	PLKGGLNTPHLHESDFSGVTPQRQVVQTPNNTVLS	TPFRTPSNGAEGLTPRSGTTPKPVINSTP	(378-439)
<i>S. pombe</i> cdc5	SVTIEVRNQLMNREQSSLLGQESIPLQPGGTGYTGVT	-PSHAANGS--	-ATP (380-434)
b-Myb	PVK-TL--PFSPSQFNLNFWNKQDTTLE	ESPSLTS	TPLHDKTPLHQKHAAF (445-503)
a-Myb	ILRKKRKMRVGHSPPGSEL-RDG	SUNDGGNMALKTPLKTPFSPSQFFNTCPGNEQLNIENPSF	(446-508)
hCdc5	GRTPPLRDKLNNINPREDGMADYSDPSYVKQMERESREH	HLRLLGLLGLPAPKNDFEIVLPENAEK	(440-500)
<i>S. pombe</i> cdc5	FRTPR-DTFSINAEEAERAGR-LASE-REN-KIRLKALRELLAKLPKNDYEL-ME-P-R-	-ME-P-R-	(435-487)
b-Myb	VTPDQKYSMDNTRHTP-TPFKNAKYGPLKPLQTPHLEDLKEVLRSEAGIELIIEDDIRP		(504-565)
a-Myb	TSTPICGQQKAL-ITTPLHKETTPKDKENVGFRTPPTI	RSSILGTPRPTPFFKNALAAQEKK	(509-569)

5' untranslated region:

GGCACGAGAGGAAGTGGGGCTTGAGTCGGTGGCCAAATCGCTGTTACTACTCTCTGAAGCTCTCGGCTGCTTCC
CGAGACACCCCTGGCCCAAG

Coding region:

1 DNA BINDING DOMAIN (—)

1 atccctcgaa ttatgtcaa qqqqqqcgta tggaggaata ccqaggatca aattctqaaa
61 ccacccggtaa taaaatatgg qaaaarcaq tggcttagga ttacccattt qctqcaraga
121 aaarcqcaaa accaqrgcaa agccagatgg tataatccc tggatccaaq cattaqaqaa
181 acagaarqgr ccagagaaga aqaaqaaaaa ctcttgcact tggccaaqtt qatqccaact
241 cactggagga ccatttcc aatatttgg aqaaacqccq cccaqrgctt aqaaacacta
301 qatatttcc tggataaaqcc tggccaaaga gacaatgaag agggaaacaac agatgatcca
361 cgaaaactta aacctggaga aatagatcca aatccagaaa caaaaaccaggc gccggcctgtat
421 ccaattgata tggatgagga tgaactttag atgcttctg aagccagagc ccgcttggct

2 NUCLEAR LOCALIZATION DOMAIN (—)

481 aatactcagg gaaagaaggc caagaggaaa qcaagagaga aacaatttgg aqaaagcaaga
541 cgtcttqctg ccctccaaaaa aaaaqagagaa cttcgagcaq ctggcataga aatttcaqaaq
601 aaaaqaaaaa ggaagagagg agttgattat aatggccqaaa tccccatttga aaaaaaqccct
661 qcccccttggtt ttatgatac ttctgaggaa aactaccaaq ctcttqacgc agatttcaagg
721 aaatttcaqac aacaggatct tggatggggag ctaagatctg aaaaqaaagg aagagataga
781 aaaaqagaca aacagcattt gaaaaggaaa aaagaatctg atttaccatc agctattctt
841 caaacttagtgc tggtttctga atttactaaa aagagaagca aacttagtact tcctgccccct
901 cagatttcag atgcagaact ccaggaagg taaaatggtag gccaagcgag tggaaatttgc
961 cgtccaaactg ccgaggaattt tggcataaca aatttgcattt ccagtagact ttgtctgag
1021 tacaatgtca ccaacaacag cgttgctttt agaacaccac gaacaccaggc ttcccaggac
1081 agaatttgc aggaagccca gaacctcatg gcccacca atgtggacac cccatttggaaa

3 ACTIVATING DOMAIN (—)

1141 ggtggactta atacccatt qcatqaaqgt dacttctcaq tggtaactcc acaqcgacaaa
1201 gttgtacaga ctccaaacac agtttctctt actccattca qgactccctt taatqgagct
1261 qaaqqqctqa ctccccqqaq tggaaacaact cccaaaccaq ttatataactc tactccqqt
1321 aqaactccctc ttccqagacaa qttaaacatt aatcccqagg atqqaatggc agactataq
1381 qatccctttt acgtqaaqca qatqaaaqga qaatcccqag aacatctccg tttagggttt
1441 ttggcccttc ctggccctaa gaatgattt gaaattgttc taccggaaaa tggcgagaag
1501 gagctggaaag aacgtgaaat agatgatact tacattgaaat atgctgctga tggatgct
1561 cggaaagcagg ccatacgaga tgcagagegt gtaaaggaaa tggaaacgaaat gcataaagct
1621 gtccagaaag atctgccaag accatcggaa gtaaatgaaa ctattctaag acccttaaat
1681 gtagaaccgc tttaacaga ttacagaaa agtgaagaac taatcaaaaa agaaatgatc
1741 acaatgttc attatgaccc ttacatcac cttatgaaac catctggaaa taaaaaggc
1801 aaaactgttag gttttgtac caataattca gagcacatta cctatcttgc acataatcc
1861 tataaaaagt tctccaaaga agagctgaaa aaggcccagg atgttttggc gcaggagatg
1921 gaagtggta aacaaggaat gagccatgaa gagctctcaa gtgaagcttta taaccagggt
1981 tggaaagaat gctacagtca agtttataat tttcttggc agagccgcta cacacgggccc
2041 aatctggcta gtaaaaaggaa cagaattgaa tcacttggaaa agaggctgaa gataaacagg
2101 ggtcacatga cgacagaagc caagagggtt gcaagatgg aaaaagat gaaaatttttgg
2161 ttgggggggtt accagtctcg tgcattgggg ctcatgaaac agttgaatgaa ctatgggac
2221 caaatttgaac aggctcactt ggagttacgc acttttggaa aactcaagaa acatgaagat
2281 tctgctatttcc cccggaggctt agagtgtcta aaagaagacg ttcaagcaca acaagaaa
2341 gaaaaggaac ttcaacatag atatgctgat ttgctgctgg agaaagagac tttaaagtca
2401 aaatttctga

3' untranslated region:

ATGACAGTTTATATCTGTACAGGATTAATTAATGCCCTTTTCACTCTAGAAGCTGAAACTG ATGTTTATCTTCATTGACA
AATTTACCCACCACTCTGGTTTTCAGTTGTTTAAATGATATGATCTACACATTCTGTGTATAAGACCTTAACTCCACA
GGACGGACATTAGAGTTAAATTATTA AGGCTATCATCTTTTGTAAATGTCATATTGCAAACTTTTGTGTTGGCTTTAA
TTTAAAGCCTAATTTAAAGTGTGCTGAGTAACCTCTGAAATAAAAACAAAATATTTAA

Fig. 2D

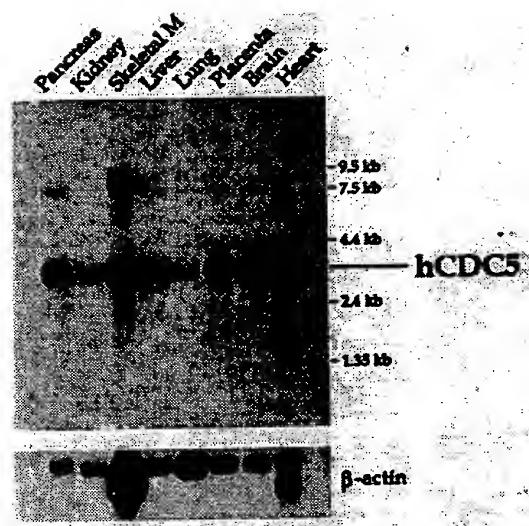


FIG. 3

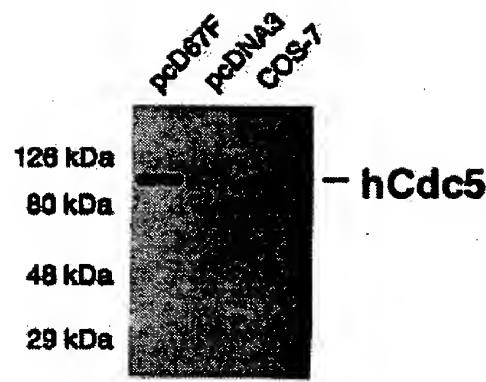


FIG. 4A

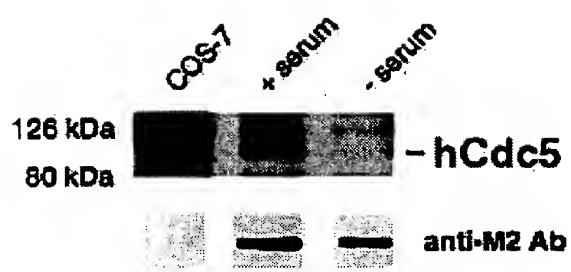


FIG. 4B

3T15.8
3T15.8.22 + Tet
3T15.8.22 - Tet x 12h
3T15.8.22 - Tet x 24h
3T15.8.22 - Tet x 36h
3T15.8.22 - Tet x 48h

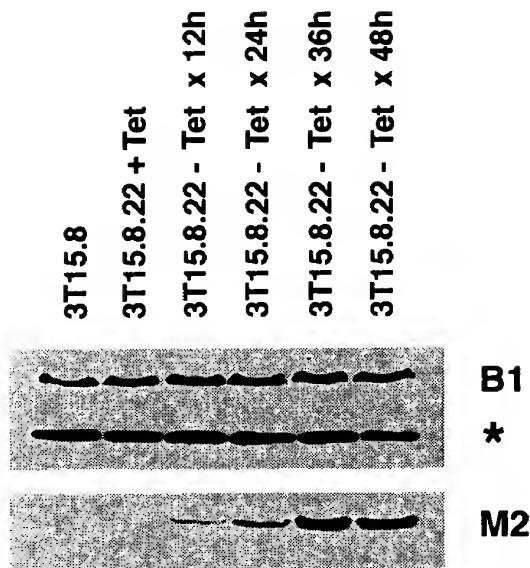


FIG. 5

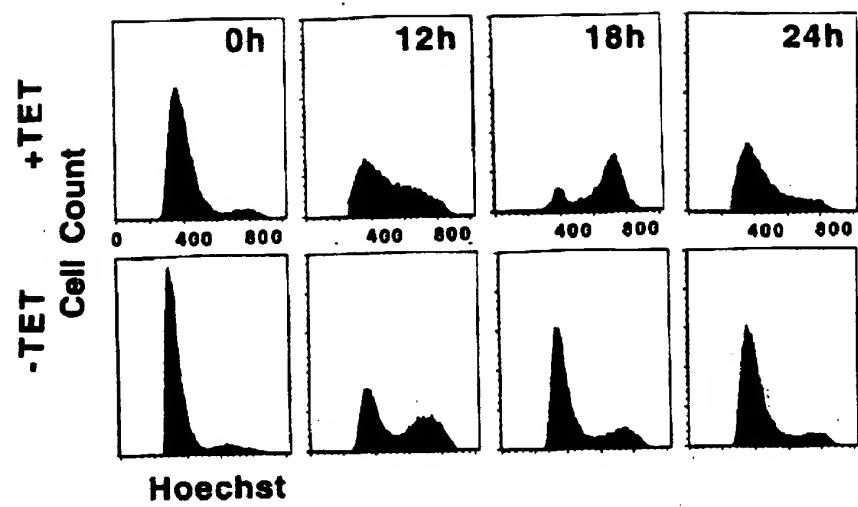


Fig. 6

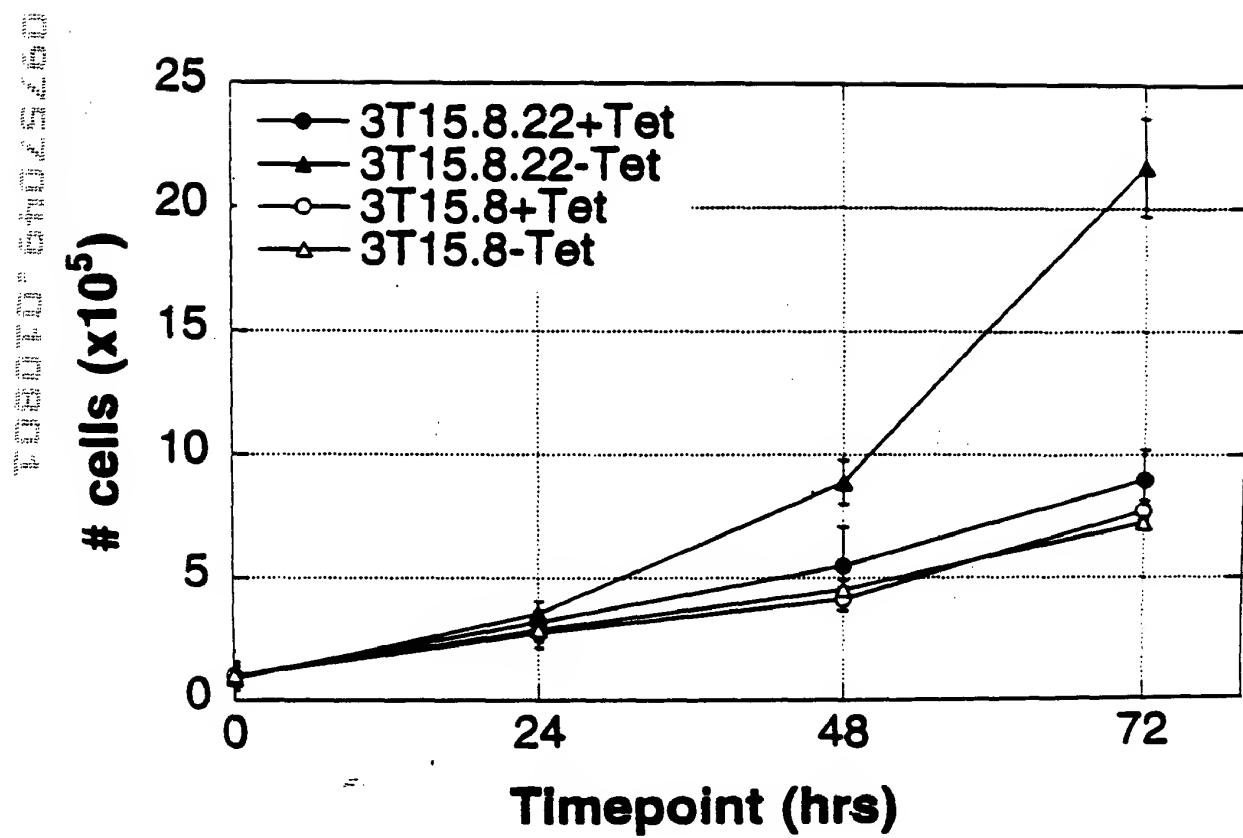


Fig. 7

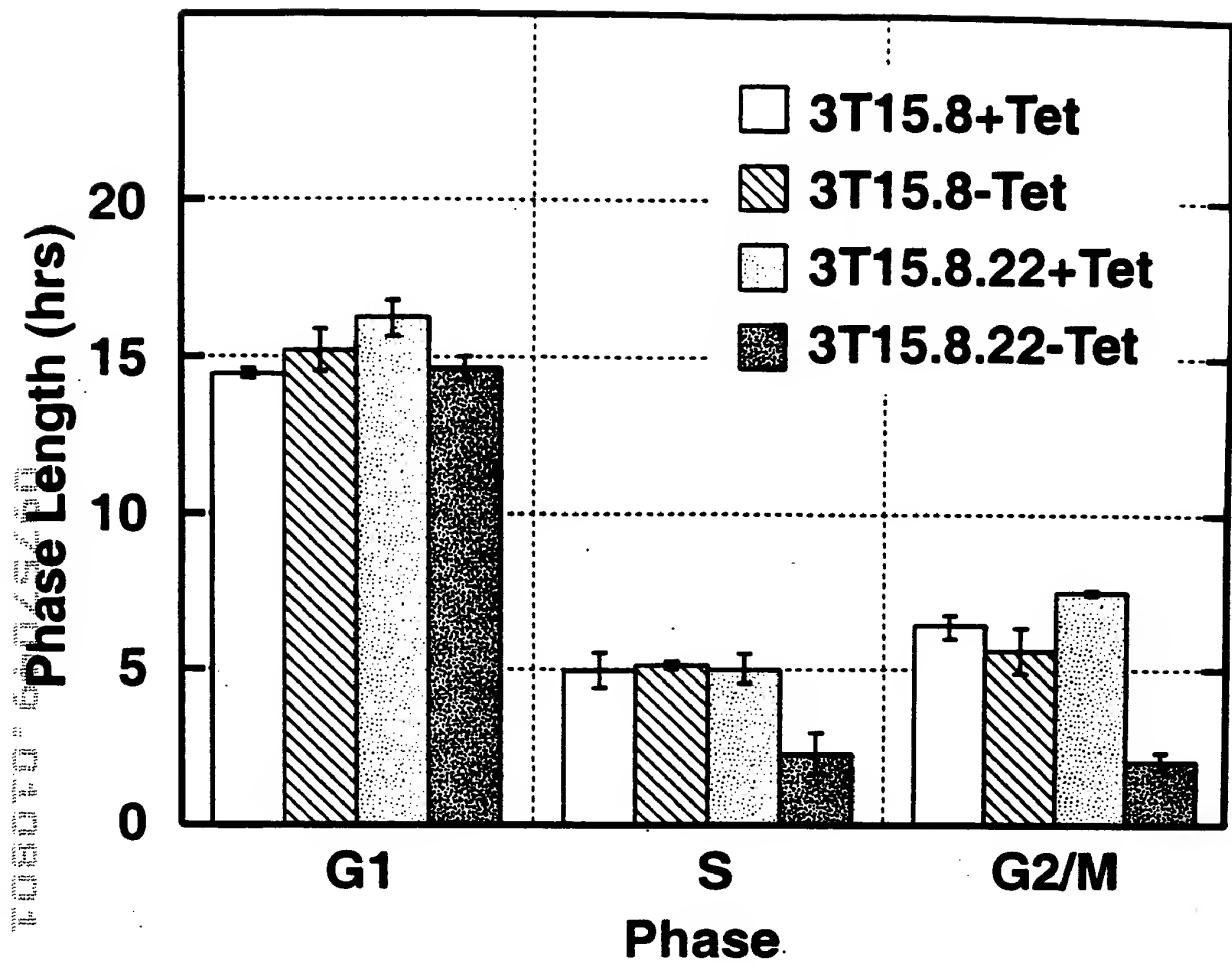


FIG. 8

Cell size by FSC
(arbitrary units)

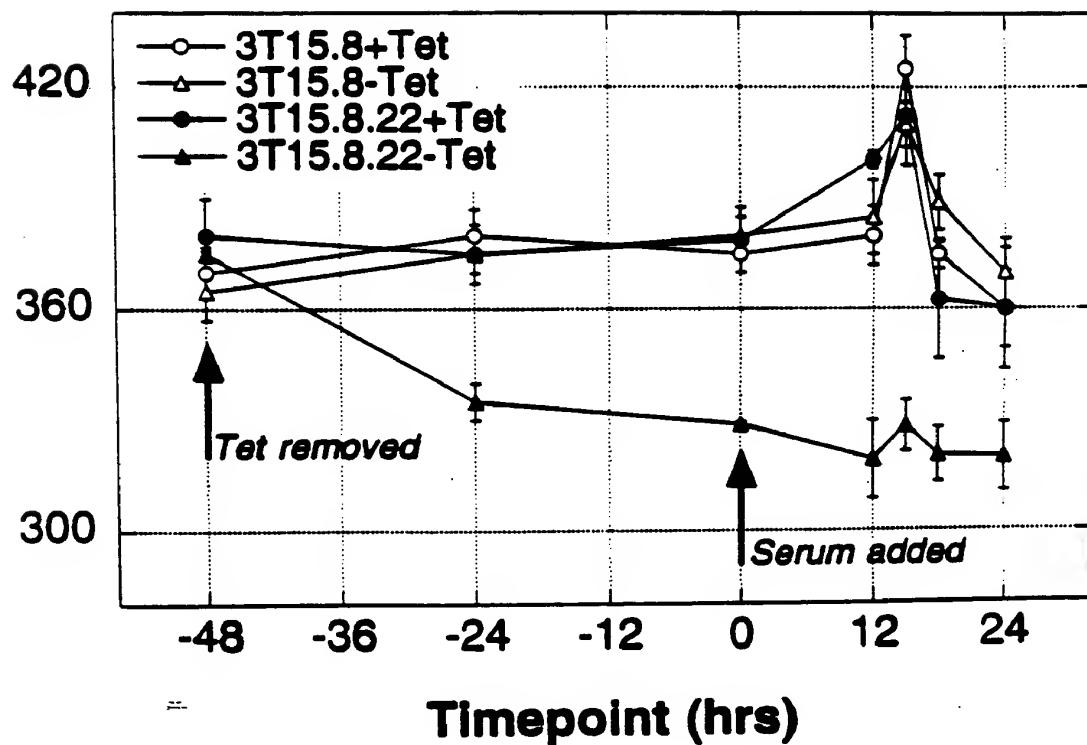


Fig. 9

hCdc5 *FLAG* NLS DOMAIN ACTIVATION DOMAIN

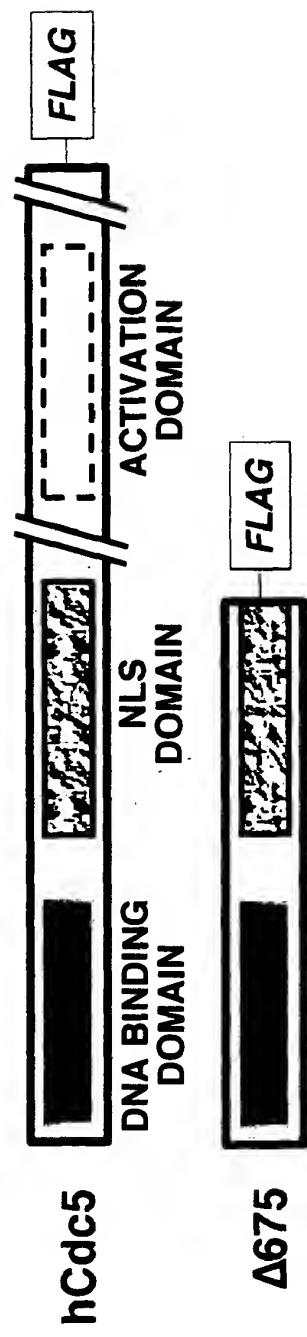


Fig. 10

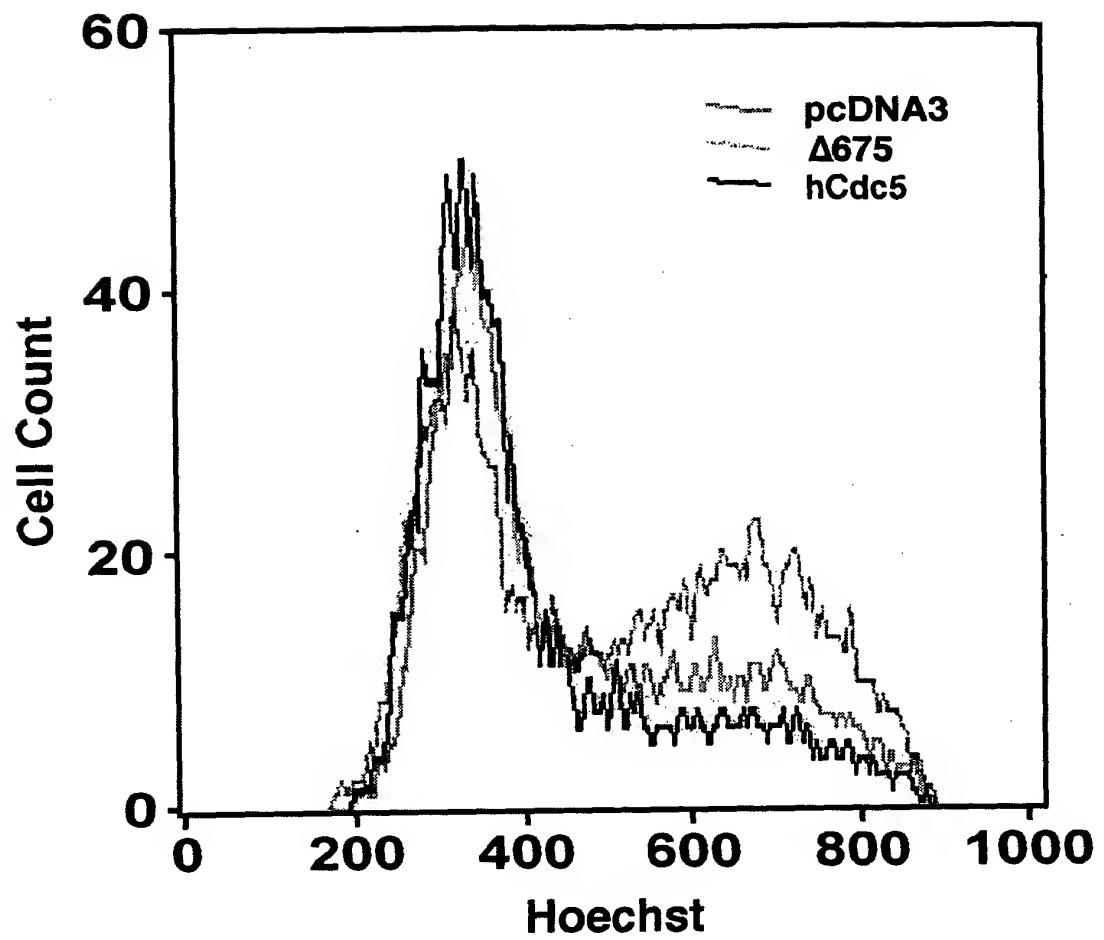


FIG. 11

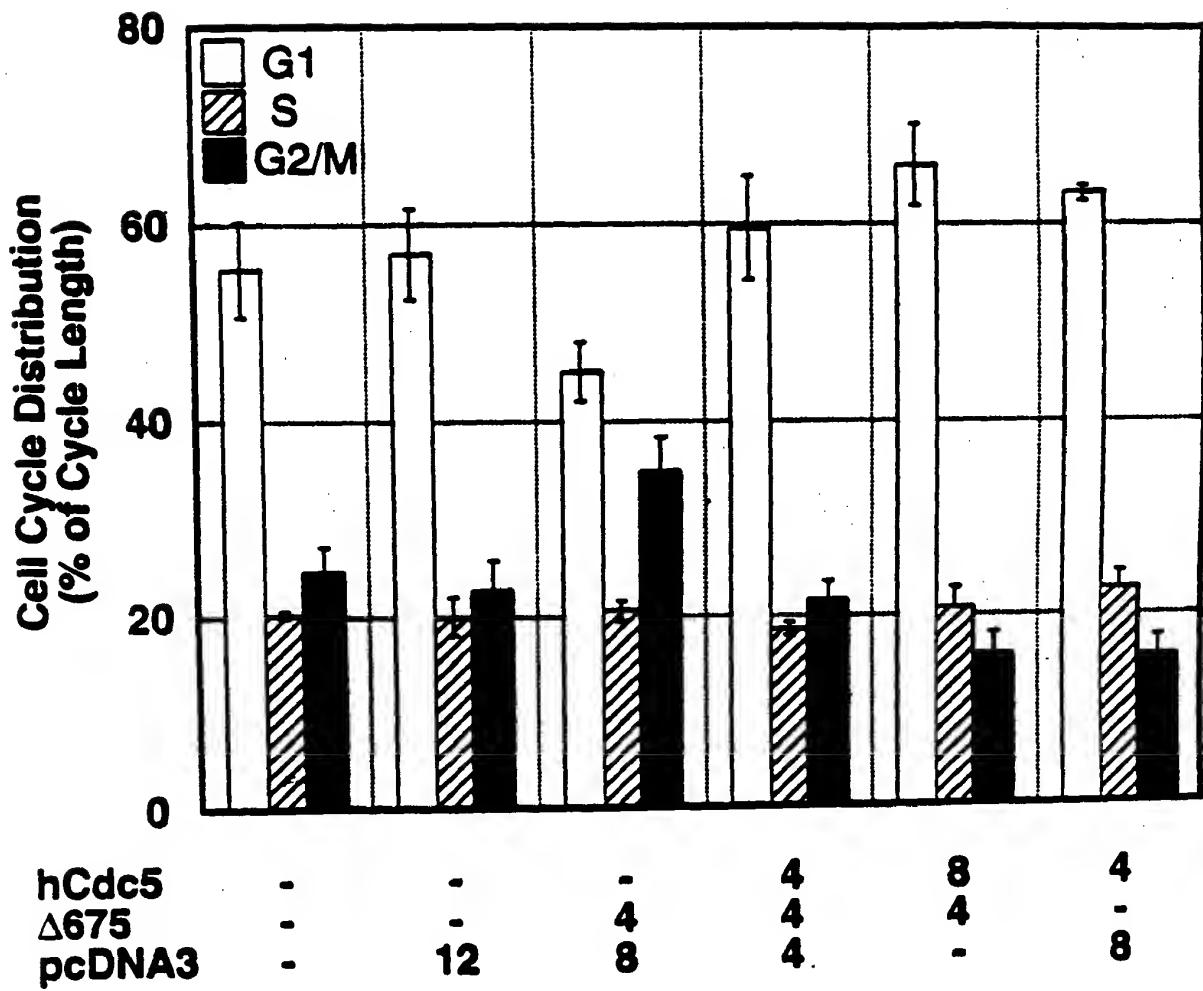


Fig. 12

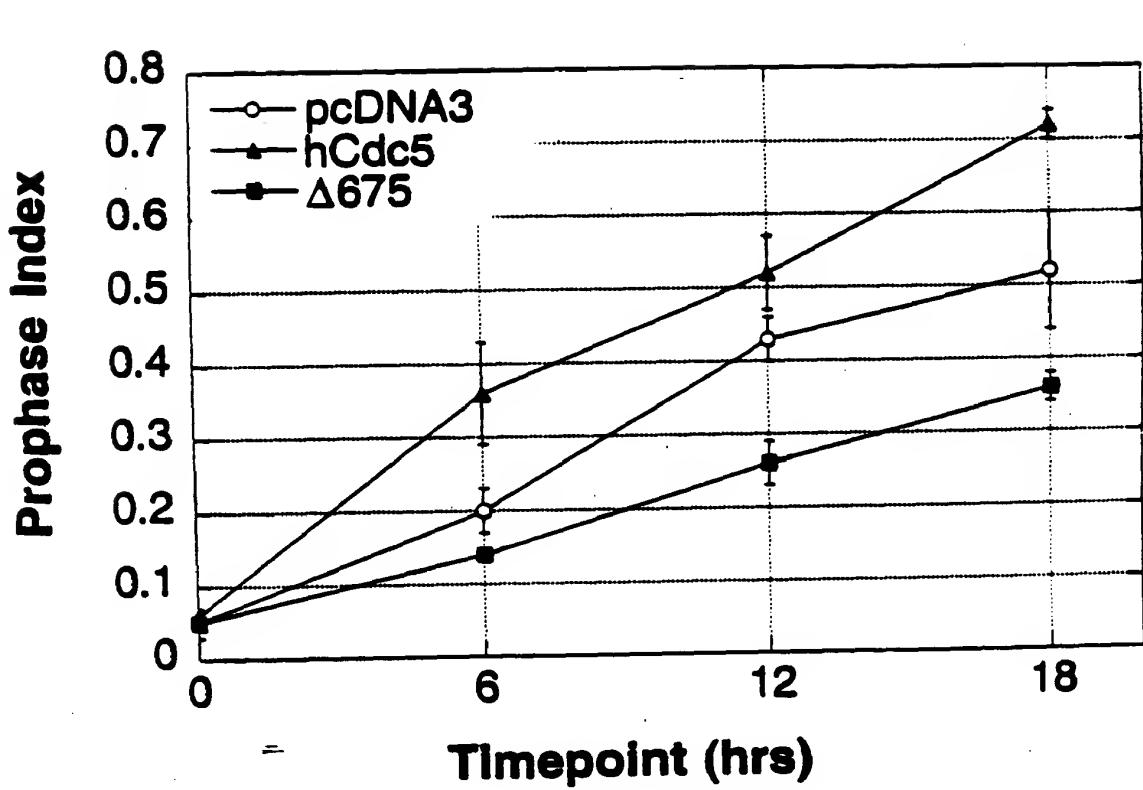
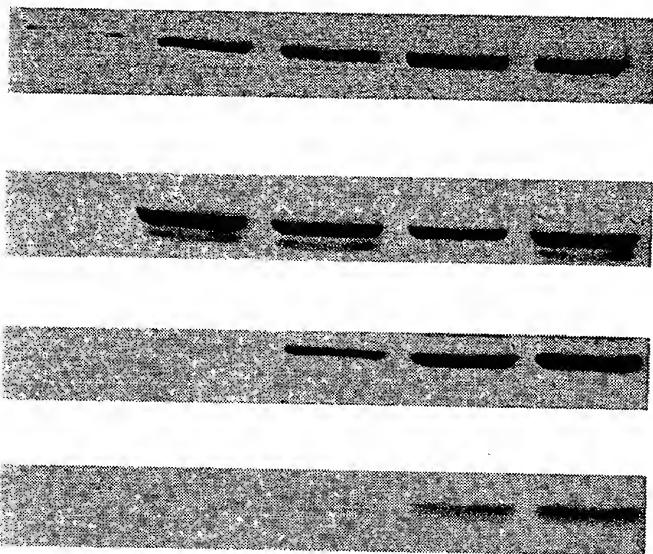


Fig. 13

0 12 15 18 21 hrs



hCdc5

p50 CLNE

p60 CLNA

p62 CLNB1

FIG. 14A

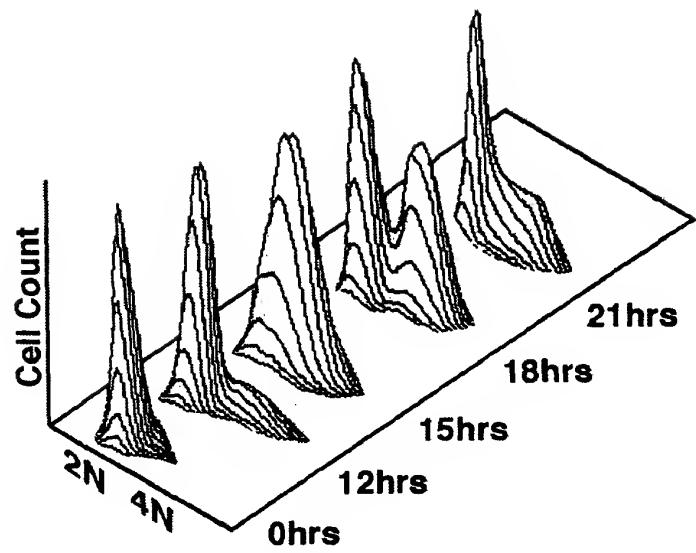


FIG. 14B

Consensus	G A T T T A A C A T A A	(SEQ ID NO:13)
8.05	G A T T T A A C A T A A	
8.04	G A T T T A A C A T A A	
8.03	G A T T T A A C A T A A	
8.02	G A T T T A A C A T A A	
8.01	G A T T T A A C A T A A	
6.05	G G T G T A A A C G T G G	(SEQ ID NO:36)
6.04	G T G T T A C C A C A T	(SEQ ID NO:37)
6.03	C C A T T A A A T T T A G	(SEQ ID NO:38)
6.02	G A G A T A A A G T C T	(SEQ ID NO:39)
6.01	G T G T T A T T G A A A	(SEQ ID NO:40)
3.05	A C C C A C G T C T A T	(SEQ ID NO:41)
3.04	G G T T A G G A T A G G	(SEQ ID NO:42)
3.03	G T T G A G T A G T A T	(SEQ ID NO:43)
3.02	C T G T T A A T T T C C	(SEQ ID NO:44)
3.01	G G T G T T A T T G A T	(SEQ ID NO:45)

FIG 15